

S-09-525-041-2 (1-158) x US-08-422-166-4 (1-522)
 quer: Match: 24.83%
 B: 24.83%
 Indels: 64
 Gaps: 16
 10 LeuleutauSerCysLeu---AlaLysThrGlyValLeuGlyAspIleIleMetArg--- 27
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 37 ATGCCTGCTTCCGCTCATGCTGTGCTGCTGCTGAGGTGAGAGACCCAGGGAA 96
 28 --Proser-----CysAlaProGlyTrpPheTyRHisLysserAsnCysTr 42
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 97 CTCGCCCTGACGGATCGCTGCTCCAAAGGCTCCAAGCCATGGCTGCTCCACTGCT 156
 43 GlyTyrHeArgLySLeuArgSerTrpSerAspAlaGluLeuGluCysGlnSerTyRg 62
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 157 GCCTTGTTTCTCACCAAATCTGGCAAGCTGCAAGTAGCAGTCAGTCAGCTGCT 216
 63 AsnGluAlaHistLeuLaaSerIleLeuSerLeuLysGluAlaSerThrIleAlaGluTyR 82
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 217 TCTGGA--AACCTGGTGTCTGCTGCTGAGTCGGCTGAGGGATCTCTGCTGCTCCCTG 273
 83 IleSerGlyTyrglnArgSerGlnPro--IleTrpIleGlyLeuHisAspProGly 101
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 274 GTGAAGAGCATGGTAACGCTACTCTACCTCTGGATGGCTCATGACCCACACAG 333
 102 ArgGlnGln-----TrpGlnTrpIleAspGlyAlaMetTyLeuTyRarg 116
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 334 GGCACCCGAGCCCAATGGAGAAGGGTGGGAGCTGACTAGCTGAGCTGATGCTG 393
 117 SerTrp-----SerGlySerMetGlyGlyAsnLysHisCysAlaGluMetSer 134
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 394 GCATGGAGGAGAAATCCCTCCACCATCTCAAGCCCCGGCACTGCGGACCTGIGGAGA 453
 135 AsnAsnAsnPhalLeuThrTrpSerSerInGluCysAsnLysArgGlnLysPhalLeuCys 154
 ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 454 AGCACAGCAATTCTGAGCTGGAAAGATTTAACTGTAGTGTAGGTACCCATGCTG 513
 155 Lys 155
 514 AAA 516

5/4 3 6/69

QLT 11
 07-778-156-12
 sequence 12: Application US/07778156
 Inventor No. 5436169
 GENERAL INFORMATION:
 APPLICANT: IOVANNA, JUAN-LUCIO
 APPLICANT: KEIM, VOLKER
 APPLICANT: DAGORN, JEAN-CHARLES
 TITLE OF INVENTION: PROTEIN ASSOCIATED WITH ACUTE
 TITLE OF INVENTION: PANCREATITIS, AGENTS FOR THE DIAGNOSIS OF ACUTE
 NUMBER OF INVENTION: PANCREATITIS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 STREET: P.C.
 CITY: 1755 Jefferson Davis Highway, Fourth Floor
 STATE: Arlington
 COUNTRY: Virginia
 ZIP: U.S.A.
 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07-778,156
 FILING DATE: 1991219
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 2

L3 ANSWER 58 OF 59 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN
DUPLICATE 4
AN 1993:432762 BIOSIS
DN PREV199396087387
TI A gene homologous to the **reg** gene is
expressed in the human pancreas.
AU Bartoli, Catherine; Gharib, Bouchra; Giorgi, Dominique; Sansonetti, Alice;
Dagorn, Jean-Charles; Berge-Lefranc, Jean-Louis [Reprint author]
CS Unite 315 l'INSERM, 46 Boulevard Gaye, 13258 Marseille Cedex 9, France
SO FEBS (Federation of European Biochemical Societies) Letters, (1993) Vol.
327, No. 3, pp. 289-293.
CODEN: FEBLAL. ISSN: 0014-5793.
DT Article
LA English
OS Genbank-L08010
ED Entered STN: 22 Sep 1993
Last Updated on STN: 6 Nov 1993
AB We have determined the nucleotide sequence of reg1 a **human**
genomic DNA fragment homologous to the **reg** gene which is
expressed in the exocrine pancreas and regenerating islets.
Sequence comparisons of **reg** and reg1 suggested similar
exon-intron organisation. Based on this assumption, specific
oligonucleotides for reg1 exons were used to demonstrate expression of the
reg1 gene in pancreas and liver. The proteins encoded by **reg** and
reg1 comprise 166 amino acids and differ by 22 amino acids only.

RA Okamoto H.; "Structural, chromosomal localization and expression of mouse genes encoding type III Reg, RegII alpha, RegII beta, RegII gamma.;" RT Moriuchi S., Watane M., Nakagawara K. I., Suzuki Y., RL Miyashita H., Yonekura H., Okamoto H.; CC -I. FUNCTION: MIGHT BE A STRESS PROTEIN INVOLVED IN THE CONTROL OF BACTERIAL PROLIFERATION.
 CC -! TISSUE SPECIFICITY: SMALL INTESTINE, AND PANCREAS.
 CC -! DISEASE: OVEREXPRESSED DURING THE ACUTE PHASE OF PANCREATITIS.
 CC -! SIMILARITY: Contains 1 C-type lectin family domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC
 CC EMBL; D63356 ; BAA18925_1; -.
 DR EMBL; D63357 ; BAA1892_1; -.
 DR EMBL; D63358 ; BAA18927_1; -.
 DR HSPN; P0451; ILIT.
 DR MGI; MGI:109408; Regja.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c_1.
 DR PRINTS; PRO1504; PNCREATTTSAP.
 DR SMART; SM00034; CLECT_1.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
 DR SIGNAL; Lectin; Inflammatory response; Acute phase; Multigene family.
 FT 26 BY SIMILARITY.
 FT CHAIN 175 PANCREATITIS-ASSOCIATED PROTEIN 2.
 FT DOMAIN 38 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 40 BY SIMILARITY.
 FT DISULFID 68 BY SIMILARITY.
 FT DISULFID 146 BY SIMILARITY.
 FT DISULFID 163 AA: 19539 MW: 3E311B3976EB0P11 CRC64;
 SQ SEQUENCE 175 AA:
 Query Match 27.6%; Score 242; DB 1; Length 175;
 Best Local Similarity 34.4%; Pred. No. 2.8e-17; Mismatches 64; Indels 18 16; Gaps 6; Matches 56; Conservative 27; Mismatches 64; Indels 18 16; Gaps 6; ;

RA RX
 RA RP
 RA SEQUENCE FROM N.A.
 RA MEDLINE=91153997; PubMed=8110835;
 RA MEDLINE=91315167; PubMed=8348956;
 RA Bartoli C., Gharib B., Giorgi D., Sansonetti A., Dagorn J.-C., RA Berge-LeFranc U.; "Isolation, structural determination and expression of a novel reg gene, human RegI beta.;" RT
 RL Biochim. Biophys. Acta 1217:199-202(1994).
 RL RN [2]
 RT RN
 RT MEDLINE=91315167; PubMed=8348956;
 RL RIBB. Lett. 327:289-293 (1993).
 RL RN
 RA CARBOHYDRATE-LINKAGE SITE.
 RA RX
 RA MEDLINE=91331286; PubMed=7607222;
 RA De Reggi M., Capon C., Gharib B., Wieruszewski J.M., Michel R., Fournet B.; "The glycan moiety of human pancreatic lithostathine. Structure characterization and possible pathophysiological implications.;" RT
 RA Eur. J. Biochem. 230:503-510 (1995).
 RA CC -! PTM: ALL O-LINKED GLYCANS CONSIST OF GAL-GALNAc-GAL-GALNAc.
 CC -! TERRASACCHARIDE CORE AND GET ELONGATED (MICROHETEROGENITY).
 CC -! SIMILARITY: Contains 1 C-type lectin family domain.
 CC CARBONATE PRECIPITATION. MAY BE ASSOCIATED WITH NEURONAL SPROUTING IN BRAIN, AND WITH BRAIN AND PANCREAS REGENERATION.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D17291; BRA0424_1; -.
 DR DR
 DR EMBL; D16816; BAA0491_1; -.
 DR DR
 DR EMBL; L0010; AAA18204_1; -.
 DR PIR; S34591; RGHUIB.
 DR HSSP; P05451; ILIT.
 DR GeneW; HGNC:9952; REG1B.
 DR MIN; 167771; -.
 DR GO; GO:0002828; P:cell proliferation; THS.
 DR IntP; IPR001304; Lectin_C.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00059; lectin_c_1.
 DR PRINTS; PRO1504; PNCREATTTSAP.
 DR SMART; SM00034; CLECT_1.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
 DR PROSITE; PS00041; C-TYPE LECTIN_2; 1.
 KW Glycoprotein; Signal; Lectin; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 BY SIMILARITY.
 FT CHAIN 23 166 LITHOSTATHINE 1 BETA.
 FT DOMAIN 34 164 C-TYPE LECTIN (LONG FORM).
 FT MOD_RES 23 23 PYRROLIDONE CARBOXYLIC ACID.
 FT CARBOHYD 27 27 O-LINKED (GALNAc. . .) (MUCIN TYPE).
 FT DISULFID 36 47 BY SIMILARITY.
 FT DISULFID 64 162 BY SIMILARITY.
 FT DISULFID 137 154 BY SIMILARITY.
 FT DISULFID 166 AA: 18665 MW: D1DC20E1A5EDDB8 CRC64;
 SQ SEQUENCE 166 AA:
 Query Match 27.3%; Score 240; DB 1; Length 166;
 Best Local Similarity 34.3%; Pred. No. 4.2e-17; Mismatches 57; Indels 4; Gaps 4; Matches 46; Conservative 27; Mismatches 57; Indels 4; Gaps 4; ;

Query Match 27.3%; Score 240; DB 1; Length 166;

Best Local Similarity 34.3%; Pred. No. 4.2e-17; Mismatches 57; Indels 4; Gaps 4; Matches 46; Conservative 27; Mismatches 57; Indels 4; Gaps 4; ;

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Query Match 27.3%; Score 240; DB 1; Length 166;
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Query Match 27.3%; Score 240; DB 1; Length 166;
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 Best Local Similarity 34.3%; Pred. No. 4.2e-17; Mismatches 57; Indels 4; Gaps 4; Matches 46; Conservative 27; Mismatches 57; Indels 4; Gaps 4; ;

Query Match 27.3%; Score 240; DB 1; Length 166;
 Best Local Similarity 34.3%; Pred. No. 4.2e-17; Mismatches 57; Indels 4; Gaps 4; Matches 46; Conservative 27; Mismatches 57; Indels 4; Gaps 4; ;

Query Match 27.3%; Score 240; DB 1; Length 166;
 Best Local Similarity 34.3%; Pred. No. 4.2e-17; Mismatches 57; Indels 4; Gaps 4; Matches 46; Conservative 27; Mismatches 57; Indels 4; Gaps 4; ;

Query Match 27.3%; Score 240; DB 1; Length 166;
 Best Local Similarity 34.3%; Pred. No. 4.2e-17; Mismatches 57; Indels 4; Gaps 4; Matches 46; Conservative 27; Mismatches 57; Indels 4; Gaps 4; ;

Query Match 27.3%; Score 240; DB 1; Length 166;
 Best Local Similarity 34.3%; Pred. No. 4.2e-17; Mismatches 57; Indels 4; Gaps 4; Matches 46; Conservative 27; Mismatches 57; Indels 4; Gaps 4; ;

Query Match 27.3%; Score 240; DB 1; Length 166;
 Best Local Similarity 34.3%; Pred. No. 4.2e-17; Mismatches 57; Indels 4; Gaps 4; Matches 46; Conservative 27; Mismatches 57; Ind

		Matches	50; Conservative	33; Mismatches	72; Indels	19; Gaps	5;
Db	92 STDSDSNWIGLHDPPKQRWRHSSGSLVSYKWDGTGSPSSANAGYCYASLSISCGPKKKWD 151	Qy	-1 MASRSMRLILLISCLAKTGVLSPDII-----MRPSCAPGWYHKNCYGYERK 47				
Qy	144 NECNKROHFLCKYR 157	Db	1 MAQNIVYLILFLCMLFLSISQGQAEDDFPLAKDLSAKINCPEGANAYGSYLYIBD 60				
Db	152 ESECKKSFVCKE 165	Qy	43 LRNWSDAELECOQYNGAHASLISUXEASTIAYI-SGYORSQPINGLHPQKROW 105				
RESULT 7		Db	61 RLTWGEBADLPQCOMM-NAGHLVLSOAEBSNFVASLVEKGTAASN-VWTGLHOPKSNRW 118				
ID LIT2_MOUSE STANDARD; PRT; 173 AA.	AC Q00873; DT 01-NOV-1995 (Rel. 32. Created)	Qy	106 QWIDGAMVLYRSNS--GKSMGNKHAEMISSNNFLTWSSNECNKROHFLCKYR 157				
DE DE	DT 28-FEB-2003 (Rel. 41. Last annotation update)	Db	119 HWGSGSLFLFKSWATGAPSTANRGYCIVSLSNTAYKKWDENDCEAOYSFVCKE 172				
DE (Pancreatic thread protein 2) (PPTP) (islet of langerhans regenerating	DE protein 2) (REG 2).	Qy					
DE	RP SEQUENCE FROM N.A.	Db					
RC STRAIN=C57BL/6J;	OS Mus musculus (Mouse).	Qy					
RX MEDLINE=93342029; PubMed=8340418;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Db					
RA Unno M., Yonekura H., Nakagawa K.-I., Watanabe T., Miyashita H.,	CC Mammalia; Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Qy					
RA Morizumi S., Okamoto H., Itoh T., Terada H.,	OX NCBI_TAXID=1090;	Db					
RT [1]	RT 011 NOV 1995 (Rel. 32. Last annotation update)	Qy					
RT REG2.	RT 28 FEB 2003 (Rel. 41. Last annotation update)	Db					
RT genes, reg I and reg II. A novel type of reg gene, reg II, exists in	RT "STRUCTURE, chromosomal localization, and expression of mouse reg	Qy					
RT the mouse genome.";	RT genes, reg I and reg II. A novel type of reg gene, reg II, exists in	Db					
J. Biol. Chem. 268:15974-15982(1993).	J. Biol. Chem. 268:15974-15982(1993).	Qy					
CC -!- FUNCTION: MIGHT ACT AS AN INHIBITOR OF SPONTANEOUS CALCIUM	CC CARBONATE PRECIPITATION.	Db					
CC -!- TISSUE SPECIFICITY: EXPRESSED ONLY IN REGENERATING ISLETS AND	CC NORMAL EXOCRINE PANCREAS, BUT NOT IN NORMAL PANCREATIC ISLETS.	Qy					
CC EXPRESSED STRONGER IN PANCREAS, WEAKLY IN LIVER, BUT NOT AT ALL.	CC IN GALLBLADDER.	Db					
CC -!- SIMILARITY: Contains 1 C-type lectin family domain.	CC -!- SIMILARITY: Contains 1 C-type lectin family domain.	Qy					
CC This SWISS-PROT entry is copyright. It is produced through a collaboration	CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -	Db					
CC the European Bioinformatics Institute. There are no restrictions on its	CC use by non-profit institutions as long as its content is in no way	Qy					
CC modified and this statement is not removed. Usage by and for commercial	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/	Db					
CC or send an email to license@ibb-sib.ch).	CC	Qy					
CC	CC	Db					
DR EMBL; D14011; BAA0112.1; -.	DR EMBL; D14011; BAA0112.1; -.	Qy					
DR B47148; BA7148.	DR B47148; BA7148.	Db					
DR P0451; LIT.	DR P0451; LIT.	Qy					
DR MGD; MGI:9796; REG2.	DR MGD; MGI:9796; REG2.	Db					
DR InterPro; IPR002353; AntifreezeII.	DR InterPro; IPR002353; AntifreezeII.	Qy					
DR InterPro; IPR001304; Lectin_C.	DR InterPro; IPR001304; Lectin_C.	Db					
DR InterPro; IPR00390; Pancreatitis_ac.	DR InterPro; IPR00390; Pancreatitis_ac.	Qy					
DR PFam; PF00059; Lectin_C; 1.	DR PFam; PF00059; Lectin_C; 1.	Db					
DR PRINTS; PRO1504; PNCREATITSAP.	DR PRINTS; PRO1504; PNCREATITSAP.	Qy					
DR PRINTS; PRO0556; ANTFREEZEII.	DR PRINTS; PRO0556; ANTFREEZEII.	Db					
DR SMART; SM00034; CLECT; 1.	DR SMART; SM00034; CLECT; 1.	Qy					
DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.	DR PROSITE; PS00615; C_TYPE_LECTIN_1; 1.	Db					
DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.	DR PROSITE; PS00041; C_TYPE_LECTIN_2; 1.	Qy					
DR KW Signal; Lectin.	DR KW Signal; Lectin.	Db					
PT SIGNAL; 1 22 BY SIMILARITY.	PT SIGNAL; 1 135 C-TYPE LECTIN (LONG FORM).	Qy					
PT CHAIN 23 173 LITHOSTATHINE 2.	PT DOMAIN 1 135 C-TYPE LECTIN (LONG FORM).	Db					
PT DOMAIN 41 171 C-TYPE LECTIN (LONG FORM).	PT DISULFID 3 14	Qy					
PT DISULFID 43 54 BY SIMILARITY.	PT DISULFID 31 131	Db					
PT DISULFID 71 169 BY SIMILARITY.	PT DISULFID 38 133	Qy					
PT DISULFID 144 161 BY SIMILARITY.	PT DISULFID 106 123	Db					
PT SEQUENCE 173 AA; 19407 MW; 7D34C4DAB23225C CRC64;	PT DISULFID 86 86 INTERCHAIN.	Qy					
Query Match Score 26.9%; Score 236.5; DB 1; Length 173; Best Local Similarity 28.7%; Pred. No. 9.8e-17; Length 173; Query Match Score 26.5%; Score 233; DB 1; Length 135; Best Local Similarity 34.4%; Pred. No. 1.7e-16; Matches 45; Conservative 18; Mismatches 64; Indels 4; Gaps 2; Query Match Score 29 SCAPGMVYHKSNCYGRKLNMSDALETOSYGNGAHASLISUXEASTIAYI-SGYOR 88; 2 NCPLDWPMLGLUCYKIFNOLCTWDEAMFEMCFKPGCGCHSLPHRYGESELIAEVISDHK 61; Query Match Score 28.7%; Score 236.5; DB 1; Length 173; Best Local Similarity 28.7%; Pred. No. 9.8e-17; Length 173; Query Match Score 26.5%; Score 233; DB 1; Length 135; Best Local Similarity 34.4%; Pred. No. 1.7e-16; Matches 45; Conservative 18; Mismatches 64; Indels 4; Gaps 2; Query Match Score 29 SCAPGMVYHKSNCYGRKLNMSDALETOSYGNGAHASLISUXEASTIAYI-SGYOR 88; 2 NCPLDWPMLGLUCYKIFNOLCTWDEAMFEMCFKPGCGCHSLPHRYGESELIAEVISDHK 61;	Db						